Amendment to the Claims:

Please amend the claims as follows:

This listing of claims will replace all prior versions, and listing, of claims in the application:

Please cancel claims 1 to 41 and 56 to 92, without prejudice.

Listing of Claims:

Claims 1 to 41 (canceled)

Claim 42 (currently amended): A method of generating a variant nucleic acid comprising:

obtaining a nucleic acid comprising (a) a sequence having at least 70% sequence identity to a sequence as set forth in SEQ ID NO: 1, wherein the sequence encodes a polypeptide having amidase activity, ~~sequences substantially identical thereto, sequences complementary thereto, fragments comprising at least 30 consecutive nucleotides thereof, and fragments comprising at least 30 consecutive nucleotides of the sequences~~ or, (b) a sequence complementary to (a) [[SEQ ID NO: 1]]; and

modifying one or more nucleotides in said nucleic acid [[sequence]] to another nucleotide, deleting one or more nucleotides in said nucleic acid [[sequence]], or adding one or more nucleotides to said nucleic acid [[sequence]], thereby generating a variant nucleic acid.

Claim 43 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis (GSSM™) and any combination thereof.

Claim 44 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by error-prone PCR.

Claim 45 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by shuffling.

Claim 46 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by oligonucleotide-directed mutagenesis.

Claim 47 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by assembly PCR.

Claim 48 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by sexual PCR mutagenesis.

Claim 49 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by *in vivo* mutagenesis.

Claim 50 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by cassette mutagenesis.

Claim 51 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by recursive ensemble mutagenesis.

Claim 52 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by exponential ensemble mutagenesis.

Claim 53 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by site-specific mutagenesis.

Claim 54 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by gene reassembly.

Claim 55 (currently amended): The method of claim 42, wherein the modifications, deletions or additions are introduced by gene site saturated mutagenesis (GSSM™).

Claims 56 to 92 (canceled)

Claim 93 (new): A method of generating a variant nucleic acid comprising:

obtaining a nucleic acid comprising (a) at least 30 consecutive nucleotides of a sequence having at least 70% sequence identity to a sequence as set forth in SEQ ID NO:1, wherein the sequence encodes a polypeptide having amidase activity, or, (b) a sequence complementary to (a); and

modifying one or more nucleotides in the nucleic acid to another nucleotide, deleting one or more nucleotides in the nucleic acid, or adding one or more nucleotides to the nucleic acid, thereby generating a variant nucleic acid.

Claim 94 (new): The method of claim 93, wherein the nucleic acid comprises at least 40 consecutive nucleotides.

Claim 95 (new): The method of claim 94, wherein the nucleic acid comprises at least 50 consecutive nucleotides.

Claim 96 (new): The method of claim 95, wherein the nucleic acid comprises at least 75 consecutive nucleotides.

Claim 97 (new): The method of claim 96, wherein the nucleic acid comprises at least 100 consecutive nucleotides.

Claim 98 (new): The method of claim 97, wherein the nucleic acid comprises at least 150 consecutive nucleotides.

Claim 99 (new): The method of claim 93, wherein the modifications, deletions or additions are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis (GSSM™) and any combination thereof.

Claim 100 (new): A method of generating a variant nucleic acid comprising:

obtaining a nucleic acid comprising (a) a sequence encoding a polypeptide having an amidase activity, wherein the polypeptide at least 70% sequence identity to SEQ ID NO:2, or, (b) a sequence complementary to (a); and

modifying one or more nucleotides in the nucleic acid to another nucleotide, deleting one or more nucleotides in the nucleic acid, or adding one or more nucleotides to the nucleic acid, thereby generating a variant nucleic acid.

Claim 101 (new): The method of claim 100, wherein the modifications, deletions or additions are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis (GSSM™) and any combination thereof.

Claim 102 (new): The method of claim 42, wherein the sequence has at least 80% sequence identity to a sequence as set forth in SEQ ID NO:1.

Claim 103 (new): The method of claim 102, wherein the sequence has at least 90% sequence identity to a sequence as set forth in SEQ ID NO:1.

Claim 104 (new): The method of claim 103, wherein the sequence has at least 95% sequence identity to a sequence as set forth in SEQ ID NO:1.

Claim 105 (new): The method of claim 104, wherein the sequence is SEQ ID NO:1.

Claim 106 (new): A method of generating a variant nucleic acid comprising:

obtaining a nucleic acid comprising (a) a polynucleotide capable of hybridizing under stringent conditions to a nucleic acid having a sequence as set forth in SEQ ID NO:1, wherein the sequence encodes a polypeptide having amidase activity, or, (b) a sequence complementary to (a); and

modifying one or more nucleotides in the nucleic acid to another nucleotide, deleting one or more nucleotides in the nucleic acid, or adding one or more nucleotides to the nucleic acid, thereby generating a variant nucleic acid.